

1646

ENTERED



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/643,627

DATE: 01/21/2004

TIME: 14:30:11

Input Set : N:\CrF3\RULE60\10643627.RAW.txt

Output Set: N:\CRF4\01212004\J643627.raw

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1 <110> APPLICANT: Sundelin, Johan
2   Scarborough, Robert M.
3 <120> TITLE OF INVENTION: Recombinant C140 Receptor, Its Agonists and Antagonists, and
4   Nucleic Acids Encoding the Receptor
5 <130> FILE REFERENCE: 44481-5006-09-US
6 <140> CURRENT APPLICATION NUMBER: 10/643,627
7 <141> CURRENT FILING DATE: 2003-08-19
8 <150> PRIOR APPLICATION NUMBER: US/10/127,691
9 <151> PRIOR FILING DATE: 2002-04-23
10 <150> PRIOR APPLICATION NUMBER: US 08/097,938
11 <151> PRIOR FILING DATE: 1993-07-26
12 <150> PRIOR APPLICATION NUMBER: US 08/390,301
13 <151> PRIOR FILING DATE: 1995-01-25
14 <150> PRIOR APPLICATION NUMBER: US 08/474,414
15 <151> PRIOR FILING DATE: 1995-06-07
16 <160> NUMBER OF SEQ ID NOS: 63
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1475
21 <212> TYPE: DNA
22 <213> ORGANISM: Mus musculus
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (232)..(1416)
26 <223> OTHER INFORMATION: C140 receptor, genomic DNA and deduced protein
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31   acacaagaat tagacttcaa cgcgcaccaa ctgccctgtg taggacgggc ggtcactgaa 180
32   agagaatatt gtctgcaata ctctaatac atctgtctgt gttcatctga a atg ttc 237
33                                     Met Phe
34                                     1
35   cat tta aaa cac agc agc ctt act gtt gga cca ttt atc tca gta atg 285
36   His Leu Lys His Ser Ser Leu Thr Val Gly Pro Phe Ile Ser Val Met
37           5                10                15
38   att ctg ctc cgc ttt ctt tgt aca gga cgc aac aac agt aaa gga aga 333
39   Ile Leu Leu Arg Phe Leu Cys Thr Gly Arg Asn Asn Ser Lys Gly Arg
40           20                25                30
41   agt ctt att ggc aga tta gaa acc cag cct cca atc act ggg aaa ggg 381
42   Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro Ile Thr Gly Lys Gly
43           35                40                45                50
44   gtt ccg gta gaa cca ggc ttt tcc atc gat gag ttc tct gcg tcc atc 429

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45	Val	Pro	Val	Glu	Pro	Gly	Phe	Ser	Ile	Asp	Glu	Phe	Ser	Ala	Ser	Ile	
46					55					60					65		
47	ctc	acc	ggg	aag	ctg	acc	acg	gtc	ttt	ctt	ccg	gtc	gtc	tac	att	att	477
48	Leu	Thr	Gly	Lys	Leu	Thr	Thr	Val	Phe	Leu	Pro	Val	Val	Tyr	Ile	Ile	
49				70					75					80			
50	gtg	ttt	gtg	att	ggt	ttg	ccc	agt	aat	ggc	atg	gcc	ctc	tgg	atc	ttc	525
51	Val	Phe	Val	Ile	Gly	Leu	Pro	Ser	Asn	Gly	Met	Ala	Leu	Trp	Ile	Phe	
52			85					90					95				
53	ctt	ttc	cga	acg	aag	aag	aaa	cac	ccc	gcc	gtg	att	tac	atg	gcc	aac	573
54	Leu	Phe	Arg	Thr	Lys	Lys	Lys	His	Pro	Ala	Val	Ile	Tyr	Met	Ala	Asn	
55		100					105					110					
56	ctg	gcc	ttg	gcc	gac	ctc	ctc	tct	gtc	atc	tgg	ttc	ccc	ctg	aag	atc	621
57	Leu	Ala	Leu	Ala	Asp	Leu	Leu	Ser	Val	Ile	Trp	Phe	Pro	Leu	Lys	Ile	
58		115				120					125				130		
59	tcc	tac	cac	cta	cat	ggc	aac	aac	tgg	gtc	tac	ggg	gag	gcc	ctg	tgc	669
60	Ser	Tyr	His	Leu	His	Gly	Asn	Asn	Trp	Val	Tyr	Gly	Glu	Ala	Leu	Cys	
61				135					140					145			
62	aag	gtg	ctc	att	ggc	ttt	ttc	tat	ggt	aac	atg	tat	tgc	tcc	atc	ctc	717
63	Lys	Val	Leu	Ile	Gly	Phe	Phe	Tyr	Gly	Asn	Met	Tyr	Cys	Ser	Ile	Leu	
64			150						155				160				
65	ttc	atg	acc	tgc	ctc	agc	gtg	cag	agg	tac	tgg	gtg	atc	gtg	aac	ccc	765
66	Phe	Met	Thr	Cys	Leu	Ser	Val	Gln	Arg	Tyr	Trp	Val	Ile	Val	Asn	Pro	
67			165					170					175				
68	atg	gga	cac	ccc	agg	aag	aag	gca	aac	atc	gcc	gtt	ggc	gtc	tcc	ttg	813
69	Met	Gly	His	Pro	Arg	Lys	Lys	Ala	Asn	Ile	Ala	Val	Gly	Val	Ser	Leu	
70		180					185					190					
71	gca	atc	tgg	ctc	ctg	att	ttt	ctg	gtc	acc	atc	cct	ttg	tat	gtc	atg	861
72	Ala	Ile	Trp	Leu	Leu	Ile	Phe	Leu	Val	Thr	Ile	Pro	Leu	Tyr	Val	Met	
73		195				200					205				210		
74	aag	cag	acc	atc	tac	att	cca	gca	ttg	aac	atc	acc	acc	tgt	cac	gat	909
75	Lys	Gln	Thr	Ile	Tyr	Ile	Pro	Ala	Leu	Asn	Ile	Thr	Thr	Cys	His	Asp	
76			215						220					225			
77	gtg	ctg	cct	gag	gag	gta	ttg	gtg	ggg	gac	atg	ttc	aat	tac	ttc	ctc	957
78	Val	Leu	Pro	Glu	Glu	Val	Leu	Val	Gly	Asp	Met	Phe	Asn	Tyr	Phe	Leu	
79			230						235				240				
80	tca	ctg	gcc	att	gga	gtc	ttc	ctg	ttc	ccg	gcc	ctc	ctt	act	gca	tct	1005
81	Ser	Leu	Ala	Ile	Gly	Val	Phe	Leu	Phe	Pro	Ala	Leu	Leu	Thr	Ala	Ser	
82			245				250						255				
83	gcc	tac	gtg	ctc	atg	atc	aag	acg	ctc	cgc	tct	tct	gct	atg	gat	gaa	1053
84	Ala	Tyr	Val	Leu	Met	Ile	Lys	Thr	Leu	Arg	Ser	Ser	Ala	Met	Asp	Glu	
85		260					265					270					
86	cac	tca	gag	aac	aaa	agg	cag	agg	gct	atc	cga	ctc	atc	atc	acc	gtg	1101
87	His	Ser	Glu	Lys	Lys	Arg	Gln	Arg	Ala	Ile	Arg	Leu	Ile	Ile	Thr	Val	
88		275				280					285				290		
89	ctg	gcc	atg	tac	ttc	atc	tgc	ttt	gct	cct	agc	aac	ctt	ctg	ctc	gta	1149
90	Leu	Ala	Met	Tyr	Phe	Ile	Cys	Phe	Ala	Pro	Ser	Asn	Leu	Leu	Leu	Val	
91			295						300				305				
92	gtg	cat	tat	ttc	cta	atc	aaa	acc	cag	agg	cag	agc	cac	gtc	tac	gcc	1197
93	Val	His	Tyr	Phe	Leu	Ile	Lys	Thr	Gln	Arg	Gln	Ser	His	Val	Tyr	Ala	

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Input Set : N:\Crif3\RULE60\10643627.RAW.txt

Output Set: N:\CRF4\01212004\J643627.raw

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94          310          315          320
95   ctc tac ctt gtc gcc ctc tgc ctg tcg acc ctc aac agc tgc ata gac   1245
96   Leu Tyr Leu Val Ala Leu Cys Leu Ser Thr Leu Asn Ser Cys Ile Asp
97          325          330          335
98   ccc ttt gtc tat tac ttt gtc tca aaa gat ttc agg gat cac gcc aga   1293
99   Pro Phe Val Tyr Tyr Phe Val Ser Lys Asp Phe Arg Asp His Ala Arg
100         340          345          350
101   aac gcg ctc ctc tgc cga agt gtc cgc act gtg aat cgc atg caa atc   1341
102   Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Asn Arg Met Gln Ile
103         355          360          365          370
104   tcg ctc agc tcc aac aag ttc tcc agg aag tcc ggc tcc tac tct tca   1389
105   Ser Leu Ser Ser Asn Lys Phe Ser Arg Lys Ser Gly Ser Tyr Ser Ser
106          375          380          385
107   agc tca acc agt gtt aaa acc tcc tac tgagctgtac ctgaggatgt   1436
108   Ser Ser Thr Ser Val Lys Thr Ser Tyr
109          390          395
110   caagcctgct tgatgatgat gatgatgatg gtgtgtgtg   1475
112 <210> SEQ ID NO: 2
113 <211> LENGTH: 395
114 <212> TYPE: PRT
115 <213> ORGANISM: Mus musculus
116 <400> SEQUENCE: 2
117   Met Phe His Leu Lys His Ser Ser Leu Thr Val Gly Pro Phe Ile Ser
118       1          5          10          15
119   Val Met Ile Leu Leu Arg Phe Leu Cys Thr Gly Arg Asn Asn Ser Lys
120          20          25          30
121   Gly Arg Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro Ile Thr Gly
122          35          40          45
123   Lys Gly Val Pro Val Glu Pro Gly Phe Ser Ile Asp Glu Phe Ser Ala
124          50          55          60
125   Ser Ile Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Val Val Tyr
126          65          70          75          80
127   Ile Ile Val Phe Val Ile Gly Leu Pro Ser Asn Gly Met Ala Leu Trp
128          85          90          95
129   Ile Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile Tyr Met
130          100          105          110
131   Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe Pro Leu
132          115          120          125
133   Lys Ile Ser Tyr His Leu His Gly Asn Asn Trp Val Tyr Gly Glu Ala
134          130          135          140
135   Leu Cys Lys Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr Cys Ser
136          145          150          155          160
137   Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val Ile Val
138          165          170          175
139   Asn Pro Met Gly His Pro Arg Lys Lys Ala Asn Ile Ala Val Gly Val
140          180          185          190
141   Ser Leu Ala Ile Trp Leu Leu Ile Phe Leu Val Thr Ile Pro Leu Tyr
142          195          200          205
143   Val Met Lys Gln Thr Ile Tyr Ile Pro Ala Leu Asn Ile Thr Thr Cys

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144          210          215          220
145 His Asp Val Leu Pro Glu Glu Val Leu Val Gly Asp Met Phe Asn Tyr
146 225          230          235          240
147 Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Leu Leu Thr
148          245          250          255
149 Ala Ser Ala Tyr Val Leu Met Ile Lys Thr Leu Arg Ser Ser Ala Met
150          260          265          270
151 Asp Glu His Ser Glu Lys Lys Arg Gln Arg Ala Ile Arg Leu Ile Ile
152          275          280          285
153 Thr Val Leu Ala Met Tyr Phe Ile Cys Phe Ala Pro Ser Asn Leu Leu
154          290          295          300
155 Leu Val Val His Tyr Phe Leu Ile Lys Thr Gln Arg Gln Ser His Val
156 305          310          315          320
157 Tyr Ala Leu Tyr Leu Val Ala Leu Cys Leu Ser Thr Leu Asn Ser Cys
158          325          330          335
159 Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser Lys Asp Phe Arg Asp His
160          340          345          350
161 Ala Arg Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Asn Arg Met
162          355          360          365
163 Gln Ile Ser Leu Ser Ser Asn Lys Phe Ser Arg Lys Ser Gly Ser Tyr
164          370          375          380
165 Ser Ser Ser Ser Thr Ser Val Lys Thr Ser Tyr
166          385          390          395
168 <210> SEQ ID NO: 3
169 <211> LENGTH: 1255
170 <212> TYPE: DNA
171 <213> ORGANISM: Homo sapiens
172 <220> FEATURE:
173 <221> NAME/KEY: CDS
174 <222> LOCATION: (56)..(1249)
175 <223> OTHER INFORMATION: C140 receptor, genomic DNA and deduced protein
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178 cgctccaggc ctgggtgaca gcgagaccct gtctcataaa ttaaaaaatg aataa atg 58
179 Met
180 1
181 aat gta ctt tca ttt gaa caa acc agt gtt act gct gaa aca ttt att 106
182 Asn Val Leu Ser Phe Glu Gln Thr Ser Val Thr Ala Glu Thr Phe Ile
183          5          10          15
184 tct gta atg acc ctt gtc ttc ctt tct tgt aca gga acc aat aga tcc 154
185 Ser Val Met Thr Leu Val Phe Leu Ser Cys Thr Gly Thr Asn Arg Ser
186          20          25          30
187 tct aaa gga aga agc ctt att ggt aag gtt gat ggc aca tcc cac gtc 202
188 Ser Lys Gly Arg Ser Leu Ile Gly Lys Val Asp Gly Thr Ser His Val
189          35          40          45
190 act gga aaa gga gtt aca gtt gaa aca gtc ttt tct gtg gat gag ttt 250
191 Thr Gly Lys Gly Val Thr Val Glu Thr Val Phe Ser Val Asp Glu Phe
192          50          55          60          65
193 tct gca tct gtc ctc act gga aaa ctg acc act gtc ttc ctt cca att 298

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Input Set : N:\Crif3\RULE60\10643627.RAW.txt

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194	Ser	Ala	Ser	Val	Leu	Thr	Gly	Lys	Leu	Thr	Thr	Val	Phe	Leu	Pro	Ile	
195					70					75					80		
196	gtc	tac	aca	att	gtg	ttt	gtg	gtg	ggg	ttg	cca	agt	aac	ggc	atg	gcc	346
197	Val	Tyr	Thr	Ile	Val	Phe	Val	Val	Gly	Leu	Pro	Ser	Asn	Gly	Met	Ala	
198				85					90					95			
199	ctg	tgg	gtc	ttt	ctt	ttc	cga	act	aag	aag	aag	cac	cct	gct	gtg	att	394
200	Leu	Trp	Val	Phe	Leu	Phe	Arg	Thr	Lys	Lys	Lys	His	Pro	Ala	Val	Ile	
201			100					105					110				
202	tac	atg	gcc	aat	ctg	gcc	ttg	gct	gac	ctc	ctc	tct	gtc	atc	tgg	ttc	442
203	Tyr	Met	Ala	Asn	Leu	Ala	Leu	Ala	Asp	Leu	Leu	Ser	Val	Ile	Trp	Phe	
204		115					120					125					
205	ccc	ttg	aag	att	gcc	tat	cac	ata	cat	ggc	aac	aac	tgg	att	tat	ggg	490
206	Pro	Leu	Lys	Ile	Ala	Tyr	His	Ile	His	Gly	Asn	Asn	Trp	Ile	Tyr	Gly	
207	130					135				140					145		
208	gaa	gct	ctt	tgt	aat	gtg	ctt	att	ggc	ttt	ttc	tat	ggc	aac	atg	tac	538
209	Glu	Ala	Leu	Cys	Asn	Val	Leu	Ile	Gly	Phe	Phe	Tyr	Gly	Asn	Met	Tyr	
210				150					155				160				
211	tgt	tcc	att	ctc	ttc	atg	acc	tgc	ctc	agt	gtg	cag	agg	tat	tgg	gtc	586
212	Cys	Ser	Ile	Leu	Phe	Met	Thr	Cys	Leu	Ser	Val	Gln	Arg	Tyr	Trp	Val	
213				165				170				175					
214	atc	gtg	aac	ccc	atg	ggg	cac	tcc	agg	aag	aag	gca	aac	att	gcc	att	634
215	Ile	Val	Asn	Pro	Met	Gly	His	Ser	Arg	Lys	Lys	Ala	Asn	Ile	Ala	Ile	
216		180					185					190					
217	ggc	atc	tcc	ctg	gca	ata	tgg	ctg	ctg	att	ctg	ctg	gtc	acc	atc	cct	682
218	Gly	Ile	Ser	Leu	Ala	Ile	Trp	Leu	Leu	Ile	Leu	Leu	Val	Thr	Ile	Pro	
219		195				200				205							
220	ttg	tat	gtc	gtg	aag	cag	acc	atc	ttc	att	cct	gcc	ctg	aac	atc	acg	730
221	Leu	Tyr	Val	Val	Lys	Gln	Thr	Ile	Phe	Ile	Pro	Ala	Leu	Asn	Ile	Thr	
222	210				215				220						225		
223	acc	tgt	cat	gat	gtt	ttg	cct	gag	cag	ctc	ttg	gtg	gga	gac	atg	ttc	778
224	Thr	Cys	His	Asp	Val	Leu	Pro	Glu	Gln	Leu	Leu	Val	Gly	Asp	Met	Phe	
225				230				235				240					
226	aat	tac	ttc	ctc	tct	ctg	gcc	att	ggg	gtc	ttt	ctg	ttc	cca	gcc	ttc	826
227	Asn	Tyr	Phe	Leu	Ser	Leu	Ala	Ile	Gly	Val	Phe	Leu	Phe	Pro	Ala	Phe	
228				245				250				255					
229	ctc	aca	gcc	tct	gcc	tat	gtg	ctg	atg	atc	aga	atg	ctg	cga	tct	tct	874
230	Leu	Thr	Ala	Ser	Ala	Tyr	Val	Leu	Met	Ile	Arg	Met	Leu	Arg	Ser	Ser	
231		260					265				270						
232	gcc	atg	gat	gaa	aac	tca	gag	aag	aaa	agg	aag	agg	gcc	atc	aaa	ctc	922
233	Ala	Met	Asp	Glu	Asn	Ser	Glu	Lys	Lys	Arg	Lys	Arg	Ala	Ile	Lys	Leu	
234		275					280				285						
235	att	gtc	act	gtc	ctg	gcc	atg	tac	ctg	atc	tgc	ttc	act	cct	agt	aac	970
236	Ile	Val	Thr	Val	Leu	Ala	Met	Tyr	Leu	Ile	Cys	Phe	Thr	Pro	Ser	Asn	
237	290				295				300						305		
238	ctt	ctg	ctt	gtg	gtg	cat	tat	ttt	ctg	att	aag	agc	cag	ggc	cag	agc	1018
239	Leu	Leu	Leu	Val	Val	His	Tyr	Phe	Leu	Ile	Lys	Ser	Gln	Gly	Gln	Ser	
240				310				315				320					
241	cat	gtc	tat	gcc	ctg	tac	att	gta	gcc	ctc	tgc	ctc	tct	acc	ctt	aac	1066
242	His	Val	Tyr	Ala	Leu	Tyr	Ile	Val	Ala	Leu	Cys	Leu	Ser	Thr	Leu	Asn	

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos. 1
Seq#:10; Xaa Pos. 1
Seq#:11; Xaa Pos. 1,2
Seq#:12; Xaa Pos. 1,2
Seq#:13; Xaa Pos. 1
Seq#:14; Xaa Pos. 1
Seq#:15; Xaa Pos. 1
Seq#:16; Xaa Pos. 1
Seq#:17; Xaa Pos. 1
Seq#:18; Xaa Pos. 1
Seq#:50; Xaa Pos. 2
Seq#:51; Xaa Pos. 2
Seq#:52; Xaa Pos. 1
Seq#:53; Xaa Pos. 1
Seq#:56; Xaa Pos. 2
Seq#:57; Xaa Pos. 2
Seq#:58; Xaa Pos. 1
Seq#:59; Xaa Pos. 1

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 3

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10643627.RAW.txt

Output Set: N:\CRF4\01212004\J643627.raw

L:513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:528 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:544 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:560 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:590 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:605 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:1008 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0
L:1023 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0
L:1039 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52 after pos.:0
L:1055 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53 after pos.:0
L:1092 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0
L:1107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:0
L:1123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0
L:1139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59 after pos.:0